

Sequence comparison
'A'

10608449Search.txt

RESULT 2
 AX086664
 LOCUS AX086664 2406 bp DNA Linear PAT 09-MAR-2001
 DEFINITION Sequence 616 from Patent WO0112659.
 ACCESSION AX086664
 VERSION AX086664.1 GI:13276007
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Wiemann, S.
 TITLE Human dna sequences
 JOURNAL Patent: WO 0112659-A 616 22-FEB-2001;
 German Human Genome Project (DE)
 FEATURES Location/Qualifiers
 source 1. .2406
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	2.64e-244	Length:	2406
Score:	3176.00	Matches:	595
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-608-449-4 (1-595) x AX086664 (1-2406)

Qy	1 MetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLysValVal	20
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Qy	21 ProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhePheArgThrArgAla	40
Db	406 CCTTTTCCCTTCATTAAAAACGAAAGCAATTACCAACCCTTCTCTAGAACCGAGCC	465
Qy	41 CysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrpLysProArgAsn	60
Db	466 TGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCCTCTGGAAGCCTCGGAAC	525
Qy	61 LeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsn	80
Db	526 CTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCCTCGACCACGCACCGACAAC	585
Qy	81 PheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysHisGluGlyProPheLysArg	100
Db	586 TTCCGGCTTCCGTTCTCTATCTTCACTACAAGCTAAGCACGAAGGACCTTCAAGCGA	645
Qy	101 LysThrCysLysGlnGluGlnThrThrGluMetThrSerCysLeuLeuGlnAsnValSer	120
Db	646 AAGACCTGTAAGCAGGAGCAAATACAGAGATGACCGAGCTGCCCTCCTCAAAATGTTCT	705
Qy	121 ProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArgLysValMetHis	140
Db	706 CCAGGGGATTATATAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGTGCA	765
Qy	141 TyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAlaValAlaIleThr	160

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10608449Search.txt

Db 766 TATGCCCTAAAGCCAGTGCACCTCCCCGGGCCCATCAGAGCCGTGGCCATCACA 825

Qy 161 ValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLysLys 180

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Qy 181 GluGlnGluAsnIleTyrSerHisLeuAspGluGluSerSerGluSerSerThrTyrThr 200

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Qy 201 AlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeuCysTyrSerSer 220

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Qy 221 LysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPheLeuGlnAspPhe 240

Db 1006 AAAGATGGCCAGAACATCACATGAATGTCGTCCAGTGTTCGCCTACTTCCTCCAGGACTTC 1065

Qy 241 CysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCysArgGluGlyGln 260

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Qy 261 ArgGluTrpValIleGlnLysIleHisGluSerGlnPheIleIleValValCysSerLys 280

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Db 1186 GGTATGAAGTACTTGTGGACAAGAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCG 1245

Qy 301 GlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLysLeuArgGlnAla 320

Db 1246 GGGAAAGGAGAGCTTCCCTGGTGGCGGTGTCAGCCATTGCCGAAAGCTCCGCCAGGCC 1305

Qy 321 LysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCys 340

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Qy 341 GluGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeuMetAspAsnLeu 360

Db 1366 GAGGGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTT 1425

Qy 361 ProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGluProGlyGlnHis 380

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Qy 381 ThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyrVal 400

Db 1486 ACGCGACAGGGCAGCAGAACACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTC 1545

Qy 401 AlaIleCysAsnMetHisGlnPheIleAspGluGluProAspTrpPheGluLysGlnPhe 420

Db 1546 GCCATTGCAACATGCACCAGTTATTGACGAGGAGCCGACTGGTTGAAAAGCAGTTC 1605

Qy 421 ValProPheHisProProLeuArgTyrArgGluProValLeuGluLysPheAspSer 440

Db 1606 GTTCCCTTCCATCCTCCACTGCGCTACCGGGAGCCAGTCTGGAGAAATTGATTGATTCG 1665

Qy 441 GlyLeuValLeuAsnAspValMetCysLysProGlyProGluSerAspPheCysLeuLys 460

Db 1666 GGCTTGGTTAAATGATGTCATGTGCAAACCAAGGGCCTGAGAGTGACTTCTGCCTAAAG 1725

Qy 461 ValGluAlaAlaValLeuGlyAlaThrGlyProAlaAspSerGlnHisGluSerGlnHis 480

*Sequence
Comparison A*

10608449Search.txt

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 Qy 501 ProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArgAspSerGlyIle 520
 Db 1846 CCCCTGCTGCACACGGTGAAAGCCGGCAGCCCTCGGACATGCCGGACTCAGGCATC 1905
 Qy 521 TyrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGluGlyLeuSerThr 540
 Db 1906 TATGACTCGTCTGTGCCCTATCCGAGCTGTCTGCCACTGATGGAAGGACTCTCGACG 1965
 Qy 541 AspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerGlyLeuGlyGlu 560
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 Qy 561 GluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCysLysAlaAspLeu 580
 Db 2026 GAGGAACCTCCTGCCCTTCCCAAGCTCCTCTCTGGGTATGCAAAGCAGATCTT 2085
 Qy 581 GlyCysArgSerTyrThrAspGluLeuHisAlaValAlaProLeu 595
 Db 2086 GGTTGCCGCAGCTACACTGATGAACCTCACGCCGTCGCCCTTG 2130

RESULT 8
 AX364573

LOCUS AX364573 2383 bp DNA linear PAT 15-FEB-2002
 DEFINITION Sequence 4 from Patent WO0208259.
 ACCESSION AX364573
 VERSION AX364573.1 GI:18696533
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Presnell, S.R., Kuestner, R.E. and Gao, Z.
 TITLE Human cytokine receptor
 JOURNAL Patent: WO 0208259-A 4 31-JAN-2002;
 ZymoGenetics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. .2383
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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